

SEQUENCE LISTING

<110> YIN, AMY

MIRAGLIA, SHERI

GODFREY, WAYNE

BUCK, DAVID

<120> HUMAN HEMTOPOIETIC STEM AND PROGENITOR CELL ANTIGEN AND METHODS FOR ITS USE

<130> AMCE-012/02US

<150> 08/842,382

<151> 1997-04-23

<150> 08/639,891

<151> 1996-04-26

<160> 2

<170> PatentIn version 3.0

<210> 1

<211> 3804

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (38) .. (2632)

<400> 1

ccaagttcta cctcatgttt ggaggatctt gctagct atg gcc ctc gta ctc ggc	55
Met Ala Leu Val Leu Gly	
1 5	
tcc ctg ttg ctg ctg ggg ctg tgc ggg aac tcc ttt tca gga ggg cag	103
Ser Leu Leu Leu Leu Gly Leu Cys Gly Asn Ser Phe Ser Gly Gly Gln	
10 15 20	
cct tca tcc aca gat gct cct aag gct tgg aat tat gaa ttg cct gca	151
Pro Ser Ser Thr Asp Ala Pro Lys Ala Trp Asn Tyr Glu Leu Pro Ala	
25 30 35	
aca aat tat gag acc caa gac tcc cat aaa gct gga ccc att ggc att	199
Thr Asn Tyr Glu Thr Gln Asp Ser His Lys Ala Gly Pro Ile Gly Ile	
40 45 50	
ctc ttt gaa cta gtg cat atc ttt ctc tat gtg gta cag ccg cgt gat	247
Leu Phe Glu Leu Val His Ile Phe Leu Tyr Val Val Gln Pro Arg Asp	
55 60 65 70	
ttc cca gaa gat act ttg aga aaa ttc tta cag aag gca tat gaa tcc	295
Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu Gln Lys Ala Tyr Glu Ser	
75 80 85	
aaa att gat tat gac aag cca gaa act gta atc tta ggt cta aag att	343
Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val Ile Leu Gly Leu Lys Ile	
90 95 100	
gtc tac tat gaa gca ggg att att cta tgc tgt gtc ctg ggg ctg ctg	391
Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys Cys Val Leu Gly Leu Leu	
105 110 115	
ttt att att ctg atg cct ctg gtg ggg tat ttc ttt tgt atg tgt cgt	439
Phe Ile Ile Leu Met Pro Leu Val Gly Tyr Phe Phe Cys Met Cys Arg	
120 125 130	
tgc tgt aac aaa tgt ggt gga gaa atg cac cag cga cag aag gaa aat	487
Cys Cys Asn Lys Cys Gly Gly Glu Met His Gln Arg Gln Lys Glu Asn	
135 140 145 150	
ggg ccc ttc ctg agg aaa tgc ttt gca atc tcc ctg ttg gtg att tgt	535
Gly Pro Phe Leu Arg Lys Cys Phe Ala Ile Ser Leu Leu Val Ile Cys	
155 160 165	
ata ata ata agc att ggc atc ttc tat ggt ttt gtg gca aat cac cag	583
Ile Ile Ile Ser Ile Gly Ile Phe Tyr Gly Phe Val Ala Asn His Gln	
170 175 180	
gta aga acc cgg atc aaa agg agt cgg aaa ctg gca gat agc aat ttc	631
Val Arg Thr Arg Ile Lys Arg Ser Arg Lys Leu Ala Asp Ser Asn Phe	
185 190 195	

aag gac ttg cga act ctc ttg aat gaa act cca gag caa atc aaa tat Lys Asp Leu Arg Thr Leu Leu Asn Glu Thr Pro Glu Gln Ile Lys Tyr 200 205 210	679
ata ttg gcc cag tac aac act acc aag gac aag gcg ttc aca gat ctg Ile Leu Ala Gln Tyr Asn Thr Thr Lys Asp Lys Ala Phe Thr Asp Leu 215 220 225 230	727
aac agt atc aat tca gtg cta gga ggc gga att ctt gac cga ctg aga Asn Ser Ile Asn Ser Val Leu Gly Gly Gly Ile Leu Asp Arg Leu Arg 235 240 245	775
ccc aac atc atc cct gtt ctt gat gag att aag tcc atg gca aca gcg Pro Asn Ile Ile Pro Val Leu Asp Glu Ile Lys Ser Met Ala Thr Ala 250 255 260	823
atc aag gag acc aaa gag gcg ttg gag aac atg aac agc acc ttg aag Ile Lys Glu Thr Lys Glu Ala Leu Glu Asn Met Asn Ser Thr Leu Lys 265 270 275	871
agc ttg cac caa caa agt aca cag ctt agc agc agt ctg acc agc gtg Ser Leu His Gln Gln Ser Thr Gln Leu Ser Ser Ser Leu Thr Ser Val 280 285 290	919
aaa act agc ctg cgg tca tct ctc aat gac cct ctg tgc ttg gtg cat Lys Thr Ser Leu Arg Ser Ser Leu Asn Asp Pro Leu Cys Leu Val His 295 300 305 310	967
cca tca agt gaa acc tgc aac agc atc aga ttg tct cta agc cag ctg Pro Ser Ser Glu Thr Cys Asn Ser Ile Arg Leu Ser Leu Ser Gln Leu 315 320 325	1015
aat agc aac cct gaa ctg agg cag ctt cca ccc gtg gat gca gaa ctt Asn Ser Asn Pro Glu Leu Arg Gln Leu Pro Pro Val Asp Ala Glu Leu 330 335 340	1063
gac aac gtt aat aac gtt ctt agg aca gat ttg gat ggc ctg gtc caa Asp Asn Val Asn Asn Val Leu Arg Thr Asp Leu Asp Gly Leu Val Gln 345 350 355	1111
cag ggc tat caa tcc ctt aat gat ata cct gac aga gta caa cgc caa Gln Gly Tyr Gln Ser Leu Asn Asp Ile Pro Asp Arg Val Gln Arg Gln 360 365 370	1159
acc acg act gtc gta gca ggt atc aaa agg gtc ttg aat tcc att ggt Thr Thr Thr Val Val Ala Gly Ile Lys Arg Val Leu Asn Ser Ile Gly 375 380 385 390	1207
tca gat atc gac aat gta act cag cgt ctt cct att cag gat ata ctc Ser Asp Ile Asp Asn Val Thr Gln Arg Leu Pro Ile Gln Asp Ile Leu 395 400 405	1255
tca gca ttc tct gtt tat gtt aat aac act gaa agt tac atc cac aga Ser Ala Phe Ser Val Tyr Val Asn Asn Thr Glu Ser Tyr Ile His Arg 410 415 420	1303
aat tta cct aca ttg gaa gag tat gat tca tac tgg tgg ctg ggt ggc	1351

Asn	Leu	Pro	Thr	Leu	Glu	Glu	Tyr	Asp	Ser	Tyr	Trp	Trp	Leu	Gly	Gly		
		425					430					435					
ctg	gtc	atc	tgc	tct	ctg	ctg	acc	ctc	atc	gtg	att	ttt	tac	tac	ctg	1399	
Leu	Val	Ile	Cys	Ser	Leu	Leu	Thr	Leu	Ile	Val	Ile	Phe	Tyr	Tyr	Leu		
	440					445					450						
ggc	tta	ctg	tgt	ggc	gtg	tgc	ggc	tat	gac	agg	cat	gcc	acc	ccg	acc	1447	
Gly	Leu	Leu	Cys	Gly	Val	Cys	Gly	Tyr	Asp	Arg	His	Ala	Thr	Pro	Thr		
455					460				465						470		
acc	cga	ggc	tgt	gtc	tcc	aac	acc	gga	ggc	gtc	ttc	ctc	atg	gtt	gga	1495	
Thr	Arg	Gly	Cys	Val	Ser	Asn	Thr	Gly	Gly	Val	Phe	Leu	Met	Val	Gly		
				475					480					485			
gtt	gga	tta	agt	ttc	ctc	ttt	tgc	tgg	ata	ttg	atg	atc	att	gtg	gtt	1543	
Val	Gly	Leu	Ser	Phe	Leu	Phe	Cys	Trp	Ile	Leu	Met	Ile	Ile	Val	Val		
			490					495					500				
ctt	acc	ttt	gtc	ttt	ggc	gca	aat	gtg	gaa	aaa	ctg	atc	tgt	gaa	cct	1591	
Leu	Thr	Phe	Val	Phe	Gly	Ala	Asn	Val	Glu	Lys	Leu	Ile	Cys	Glu	Pro		
		505					510					515					
tac	acg	agc	aag	gaa	tta	ttc	cgg	gtt	ttg	gat	aca	ccc	tac	tta	cta	1639	
Tyr	Thr	Ser	Lys	Glu	Leu	Phe	Arg	Val	Leu	Asp	Thr	Pro	Tyr	Leu	Leu		
	520					525					530						
aat	gaa	gac	tgg	gaa	tac	tat	ctc	tct	ggg	aag	cta	ttt	aat	aaa	tca	1687	
Asn	Glu	Asp	Trp	Glu	Tyr	Tyr	Leu	Ser	Gly	Lys	Leu	Phe	Asn	Lys	Ser		
535				540					545						550		
aaa	atg	aag	ctc	act	ttt	gaa	caa	gtt	tac	agt	gac	tgc	aaa	aaa	aat	1735	
Lys	Met	Lys	Leu	Thr	Phe	Glu	Gln	Val	Tyr	Ser	Asp	Cys	Lys	Lys	Asn		
				555					560						565		
aga	ggc	act	tac	ggc	act	ctt	cac	ctg	cag	aac	agc	ttc	aat	atc	agt	1783	
Arg	Gly	Thr	Tyr	Gly	Thr	Leu	His	Leu	Gln	Asn	Ser	Phe	Asn	Ile	Ser		
				570				575					580				
gaa	cat	ctc	aac	att	aat	gag	cat	act	gga	agc	ata	agc	agt	gaa	ttg	1831	
Glu	His	Leu	Asn	Ile	Asn	Glu	His	Thr	Gly	Ser	Ile	Ser	Ser	Glu	Leu		
	585					590					595						
gaa	agt	ctg	aag	gta	aat	ctt	aat	atc	ttt	ctg	ttg	ggc	gca	gca	gga	1879	
Glu	Ser	Leu	Lys	Val	Asn	Leu	Asn	Ile	Phe	Leu	Leu	Gly	Ala	Ala	Gly		
	600				605						610						
aga	aaa	aac	ctt	cag	gat	ttt	gct	gct	tgt	gga	ata	gac	aga	atg	aat	1927	
Arg	Lys	Asn	Leu	Gln	Asp	Phe	Ala	Ala	Cys	Gly	Ile	Asp	Arg	Met	Asn		
615					620					625					630		
tat	gac	agc	tac	ttg	gct	cag	act	ggc	aaa	tcc	ccc	gca	gga	gtg	aat	1975	
Tyr	Asp	Ser	Tyr	Leu	Ala	Gln	Thr	Gly	Lys	Ser	Pro	Ala	Gly	Val	Asn		
				635				640						645			
ctt	tta	tca	ttt	gca	tat	gat	cta	gaa	gca	aaa	gca	aac	agt	ttg	ccc	2023	
Leu	Leu	Ser	Phe	Ala	Tyr	Asp	Leu	Glu	Ala	Lys	Ala	Asn	Ser	Leu	Pro		

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100


```

ccaaggcaac ggcaccattg gtctctgggt agtgctttaa gaatgaacac aatcacgtta 2832
tagtccatgg tccatcacta ttcaaggatg actccctccc ttctgtcta tttttgtttt 2892
ttactttttt aactgagtt tctatttaga cactacaaca tatgggggtgt ttgttcccat 2952
tggtatgcatt tctatcaaaa ctctatcaaa tgtgatggct agattctaac atattgccat 3012
gtgtggagtg tgctgaacac acaccagttt acaggaaaga tgcattttgt gtacagtaaa 3072
cgggtgtatat accttttgtt accacagagt tttttaaaca aatgagtatt ataggacttt 3132
cttctaaatg agctaaataa gtcaccattg acttcttggt gctgttgaaa ataatccatt 3192
ttcactaaaa gtgtgtgaaa cctacagcat attcttcacg cagagatttt catctattat 3252
actttatcaa agattggcca tgttccactt ggaaatggca tgcaaaaagcc atcatagaga 3312
aacctgcgta actccatctg acaaattcaa aagagagaga gagatcttga gagagaaatg 3372
ctgttcgttc aaaagtggag ttgttttaac agatgccaat tacggtgtac agtttaacag 3432
agttttctgt tgcattagga taaacattaa ttggagtgcg gctaacaatga gtatcatcag 3492
actagtatca agtgttctaa aatgaaatat gagaagatcc tgtcacaatt cttagatctg 3552
gtgtccagca tggatgaaac ctttgagttt ggtccctaaa tttgcatgaa agcacaaggt 3612
aaatattcat ttgcttcagg agtttcatgt tggatctgtc attatcaaaa gtgatcagca 3672
atgaagaact ggtcggacaa aatttaacgt tgatgtaatg gaattccaga tgtaggcatt 3732
ccccccaggt cttttcatgt gcagattgca gttctgattc atttgaataa aaaggaactt 3792
ggaaaaaaaa aa 3804

```

<210> 2

<211> 865

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Ala Leu Val Leu Gly Ser Leu Leu Leu Gly Leu Cys Gly Asn
1           5           10          15

```

```

Ser Phe Ser Gly Gly Gln Pro Ser Ser Thr Asp Ala Pro Lys Ala Trp
          20          25          30

```


Lys Ser Met Ala Thr Ala Ile Lys Glu Thr Lys Glu Ala Leu Glu Asn
260 265 270

Met Asn Ser Thr Leu Lys Ser Leu His Gln Gln Ser Thr Gln Leu Ser
275 280 285

Ser Ser Leu Thr Ser Val Lys Thr Ser Leu Arg Ser Ser Leu Asn Asp
290 295 300

Pro Leu Cys Leu Val His Pro Ser Ser Glu Thr Cys Asn Ser Ile Arg
305 310 315 320

Leu Ser Leu Ser Gln Leu Asn Ser Asn Pro Glu Leu Arg Gln Leu Pro
325 330 335

Pro Val Asp Ala Glu Leu Asp Asn Val Asn Asn Val Leu Arg Thr Asp
340 345 350

Leu Asp Gly Leu Val Gln Gln Gly Tyr Gln Ser Leu Asn Asp Ile Pro
355 360 365

Asp Arg Val Gln Arg Gln Thr Thr Thr Val Val Ala Gly Ile Lys Arg
370 375 380

Val Leu Asn Ser Ile Gly Ser Asp Ile Asp Asn Val Thr Gln Arg Leu
385 390 395 400

Pro Ile Gln Asp Ile Leu Ser Ala Phe Ser Val Tyr Val Asn Asn Thr
405 410 415

Glu Ser Tyr Ile His Arg Asn Leu Pro Thr Leu Glu Glu Tyr Asp Ser
420 425 430

Tyr Trp Trp Leu Gly Gly Leu Val Ile Cys Ser Leu Leu Thr Leu Ile
435 440 445

Val Ile Phe Tyr Tyr Leu Gly Leu Leu Cys Gly Val Cys Gly Tyr Asp
450 455 460

Arg His Ala Thr Pro Thr Thr Arg Gly Cys Val Ser Asn Thr Gly Gly
465 470 475 480

Val Phe Leu Met Val Gly Val Gly Leu Ser Phe Leu Phe Cys Trp Ile

				485						490						495	
Leu	Met	Ile	Ile	Val	Val	Leu	Thr	Phe	Val	Phe	Gly	Ala	Asn	Val	Glu		
			500					505					510				
Lys	Leu	Ile	Cys	Glu	Pro	Tyr	Thr	Ser	Lys	Glu	Leu	Phe	Arg	Val	Leu		
		515					520					525					
Asp	Thr	Pro	Tyr	Leu	Leu	Asn	Glu	Asp	Trp	Glu	Tyr	Tyr	Leu	Ser	Gly		
	530					535					540						
Lys	Leu	Phe	Asn	Lys	Ser	Lys	Met	Lys	Leu	Thr	Phe	Glu	Gln	Val	Tyr		
545					550					555					560		
Ser	Asp	Cys	Lys	Lys	Asn	Arg	Gly	Thr	Tyr	Gly	Thr	Leu	His	Leu	Gln		
			565						570					575			
Asn	Ser	Phe	Asn	Ile	Ser	Glu	His	Leu	Asn	Ile	Asn	Glu	His	Thr	Gly		
			580					585					590				
Ser	Ile	Ser	Ser	Glu	Leu	Glu	Ser	Leu	Lys	Val	Asn	Leu	Asn	Ile	Phe		
	595						600					605					
Leu	Leu	Gly	Ala	Ala	Gly	Arg	Lys	Asn	Leu	Gln	Asp	Phe	Ala	Ala	Cys		
	610					615					620						
Gly	Ile	Asp	Arg	Met	Asn	Tyr	Asp	Ser	Tyr	Leu	Ala	Gln	Thr	Gly	Lys		
625					630					635					640		
Ser	Pro	Ala	Gly	Val	Asn	Leu	Leu	Ser	Phe	Ala	Tyr	Asp	Leu	Glu	Ala		
			645						650					655			
Lys	Ala	Asn	Ser	Leu	Pro	Pro	Gly	Asn	Leu	Arg	Asn	Ser	Leu	Lys	Arg		
		660						665					670				
Asp	Ala	Gln	Thr	Ile	Lys	Thr	Ile	His	Gln	Gln	Arg	Val	Leu	Pro	Ile		
	675						680					685					
Glu	Gln	Ser	Leu	Ser	Thr	Leu	Tyr	Gln	Ser	Val	Lys	Ile	Leu	Gln	Arg		
	690					695					700						
Thr	Gly	Asn	Gly	Leu	Leu	Glu	Arg	Val	Thr	Arg	Ile	Leu	Ala	Ser	Leu		
705					710					715					720		

Asp Phe Ala Gln Asn Phe Ile Thr Asn Asn Thr Ser Ser Val Ile Ile
725 730 735

Glu Glu Thr Lys Lys Tyr Gly Arg Thr Ile Ile Gly Tyr Phe Glu His
740 745 750

Tyr Leu Gln Trp Ile Glu Phe Ser Ile Ser Glu Lys Val Ala Ser Cys
755 760 765

Lys Pro Val Ala Thr Ala Leu Asp Thr Ala Val Asp Val Phe Leu Cys
770 775 780

Ser Tyr Ile Ile Asp Pro Leu Asn Leu Phe Trp Phe Gly Ile Gly Lys
785 790 795 800

Ala Thr Val Phe Leu Leu Pro Ala Leu Ile Phe Ala Val Lys Leu Ala
805 810 815

Lys Tyr Tyr Arg Arg Met Asp Ser Glu Asp Val Tyr Asp Asp Val Glu
820 825 830

Thr Ile Pro Met Lys Asn Met Glu Asn Gly Asn Asn Gly Tyr His Lys
835 840 845

Asp His Val Tyr Gly Ile His Asn Pro Val Met Thr Ser Pro Ser Gln
850 855 860

His
865